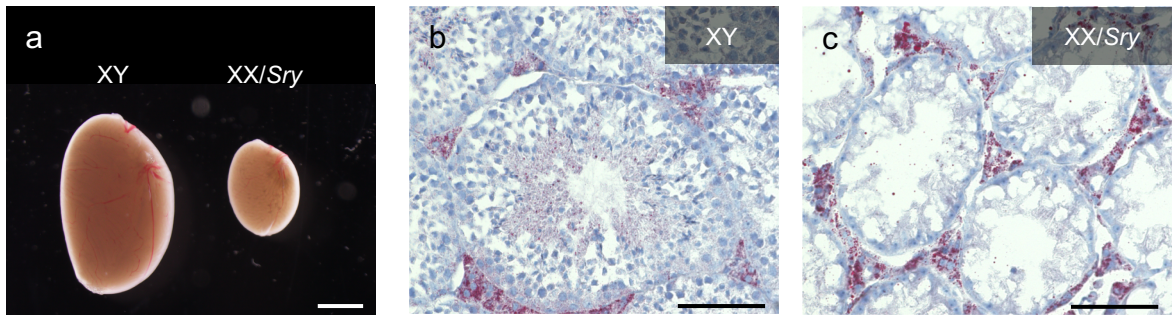


Supplemental Figures

Gene expression and functional abnormalities in XX/Sry Leydig cells

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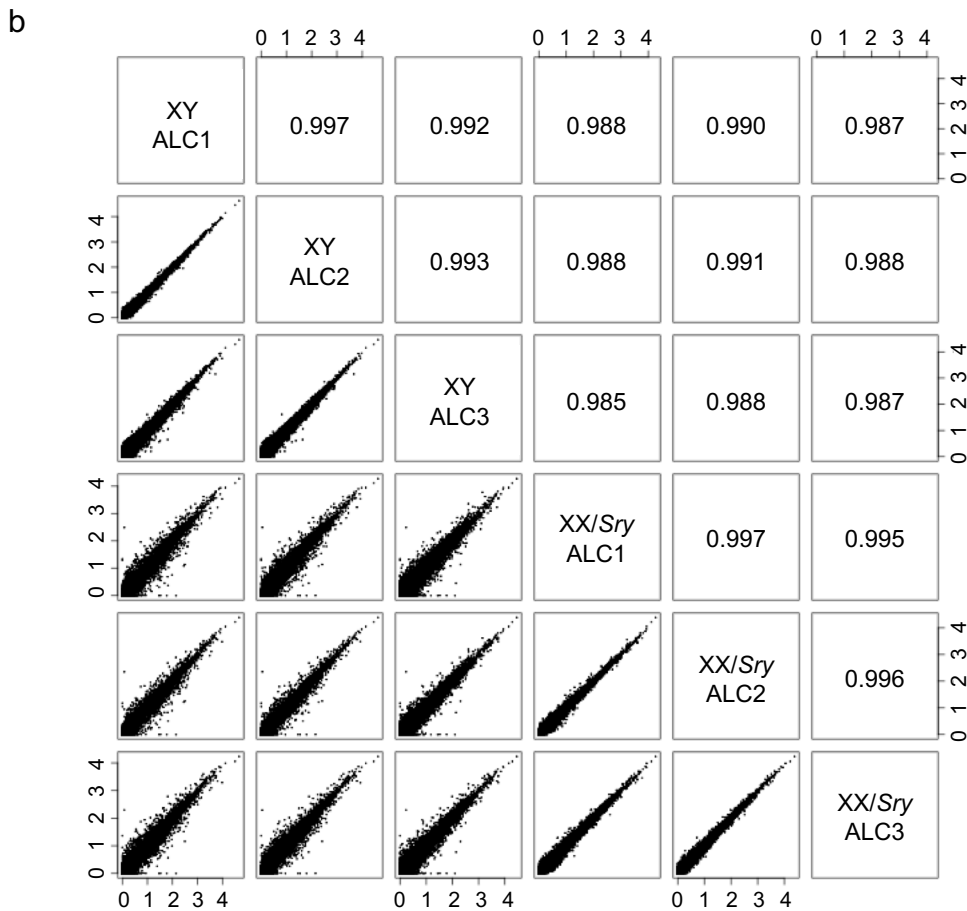


Supplemental Fig. 1, Structural differences between XY and XX/Sry testes. **a**, Whole view of XY and XX/Sry testes of eight-week-old mice are shown. Scale bar = 2 mm. **b** and **c**, XY and XX/Sry testes of eight-week-old mice were stained with Oil red O and hematoxylin. Scale bars = 50 μm.

Supplemental Fig. 1, Yanai *et al.*,

a

	Total reads	Uniquely mapped reads	Reads mapped to multiple loci
XY ALC1	12232191	11022073 (90.1%)	924025 (7.6%)
XY ALC2	22898338	20799117 (90.8%)	1653423 (7.2%)
XY ALC3	19385200	17570984 (90.6%)	1340047 (6.9%)
XX/Sry ALC1	13613624	12188410 (89.5%)	973661 (7.2%)
XX/Sry ALC2	14040206	12725129 (90.6%)	1052764 (7.5%)
XX/Sry ALC3	21150652	19238771 (91.0%)	1478237 (7.0%)



Supplemental Fig. 2, Qualities of transcriptome data. **a**, Transcriptomes were obtained from three biologically independent ALCs each for XY and XX/Sry testes. Total reads, uniquely mapped reads, and reads mapped to multiple loci are summarized for each transcriptome study. **b**, Gene expression was compared pairwise between samples. Scatter plots (log₁₀ scale) are shown upper the diagonal and correlation coefficients below the diagonal.

a Sertoli cells					b ALCs				
	Gene	CPM		Fold change		Gene	CPM		Fold change
		XY	XX/Sry				XY	XX/Sry	
PDGF	<i>Pdgfa</i>	0.8	5.2	3.44	PDGF	<i>Pdgfra</i>	247.9	431.0	1.74
	<i>Pdgfb</i>	1.2	0.5	0.71		<i>Pdgfrb</i>	0.6	2.4	2.12
	<i>Pdgfc</i>	55.9	106.3	1.88		<i>Ptch1</i>	75.2	67.8	0.90
	<i>Pdgfd</i>	0.2	0.8	1.46		<i>Ptch2</i>	0.1	1.1	1.87
Hedgehog	<i>Dhh</i>	234.4	277.8	1.18	Hedgehog	<i>Smo</i>	96.0	100.4	1.04
	<i>Ihh</i>	0.1	0.3	1.14		<i>Tgfr1</i>	43.1	39.3	0.91
	<i>Shh</i>	0.0	0.0	1.00		<i>Tgfr2</i>	2.3	3.9	1.50
	<i>Tgfb1</i>	58.9	47.9	0.82		<i>Tgfr3</i>	406.8	548.7	1.35
TGFβ	<i>Tgfb2</i>	0.5	2.8	2.55	TGFβ	<i>Fgfr1</i>	55.1	76.7	1.38
	<i>Tgfb3</i>	127.8	121.8	0.95		<i>Fgfr2</i>	180.4	173.8	0.96
	<i>Fgf2</i>	0.0	0.0	1.00		<i>Fgfr3</i>	0.1	0.2	1.12
FGF	<i>Inha</i>	1321.4	1672.8	1.27	FGF	<i>Fgfr4</i>	75.1	53.0	0.71
Activin	<i>Inhba</i>	0.1	0.7	1.52		<i>Acvr1</i>	150.9	156.2	1.03
	<i>Inhbb</i>	461.2	337.1	0.73		<i>Acvr1b</i>	6.0	7.4	1.19
IGF1	<i>Igf1</i>	1.1	5.9	3.27		<i>Acvr1c</i>	10.0	18.1	1.73
					Activin	<i>Acvr2a</i>	28.8	32.4	1.12
						<i>Acvr2b</i>	0.8	1.2	1.23
						<i>Igf1r</i>	275.8	301.9	1.09

Supplemental Fig. 3, Expression of genes related to paracrine factors. **a**, Expression of paracrine factors involved in the differentiation of ALCs was extracted from the transcriptome datasets for the XY and XX/Sry Sertoli cells. Increased and decreased gene expression in the XX/Sry Sertoli cells is indicated in red and blue, respectively, with deeper shading for larger differences. **b**, Expression of receptors for the paracrine factors was extracted from the transcriptome datasets for the XY and XX/Sry ALCs. CPMs are means of biological triplicates. Increased and decreased gene expression in the XX/Sry ALCs is indicated in red and blue, respectively, with deeper shading for larger differences.

Supplemental Fig. 3, Yanai *et al.*,

a

Gene	CPM		Fold change	Regulation	Target	Reference
	XY	XX/Sry				
<i>Cebpa</i>	80	95	1.19	Activation	<i>Star</i>	1
<i>Cebpb</i>	122	55	0.45	Activation	<i>Star</i> <i>CYP11A1</i> <i>HSD3B2</i>	1,2
<i>Creb1</i>	28	35	1.26	Activation	<i>Star</i> <i>CYP11A1</i>	1,3
<i>Fos</i>	2959	1877	0.63	Activation	<i>Star</i> <i>CYP11A1</i>	1,4
<i>Gata4</i>	200	203	1.02	Activation	<i>HSD3B1</i> <i>Cyp17a1</i>	5,6
<i>Hif1a</i>	54	61	1.12	Activation	<i>Hsd3b1</i>	7
<i>Jun</i>	1590	1389	0.87	Activation	<i>Star</i>	1
<i>Nfkb1</i>	55	54	0.99	Suppression	<i>Cyp17a1</i>	8
<i>Nfkb2</i>	27	25	0.92	Suppression	<i>Cyp17a1</i>	8
<i>Nr3b3/Esrr3</i>	24	23	0.96	Activation	<i>Cyp17a1</i>	9
<i>Nr3c1/gr</i>	44	67	1.52	Suppression	<i>Star</i>	10
<i>Nr4a1/Nur77</i>	133	123	0.92	Activation	<i>HSD3B2</i> <i>Star</i> <i>Cyp17a1</i>	10,11,12
<i>Sp1</i>	69	90	1.31	Activation	<i>Star</i> <i>CYP11A1</i> <i>Cyp17a1</i>	1,6,13
<i>Srebf1</i>	135	180	1.33	Activation	<i>Star</i>	1
<i>Yy1</i>	67	71	1.05	Activation	<i>HSD3B2</i>	14

Supplemental Fig. 4, Expression of genes encoding transcription factors. a, Expression of transcription factors involved in the regulation of steroidogenesis was extracted from the transcriptome datasets for the XY and XX/Sry ALCs. CPMs are means of biological triplicates. Increased and decreased gene expression in the XX/Sry ALCs is indicated in red and blue, respectively, with deeper shading for larger differences.

Supplemental Fig. 4, Yanai *et al.*,

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